

Sequence Alignment

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 14:04:54 ; Search time 1 Seconds
(without alignments)
6.964 Million cell updates/sec

Title: us-09-944-896-49
Perfect score: 1876
Sequence: 1 ctctttgtccaccagccca.....tcagctgaaaaaaaaa 1876

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1856 residues
Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : seq264-1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	1764.5	94.1	1856 1	us-09-790-264-1
2	25.8	1.4	1856 1	us-09-790-264-1
ALIGNMENTS				
RESULT 1				
us-09-790-264-1				
Query Match 94.1%; Score 1764.5; DB 1; Length 1856;				
Best Local Similarity 98.0%; Pred. No. 0;				
Matches 1794; Conservative 0; Mismatches 10; Indels 27; Gaps 1;				
QY	46	GCTCCATCCAGCTGAGAACACAGCCGGGTGGCTGAGCCAGGCTGTGCAGGAGCACCTG	105	
DB	18	GCTCCATCCAGCTGAGAACACAGCCGGGTGGCTGAGCCAGGCTGTGCAGGAGTGCCTG	77	
QY	106	ACGGGCCCCAACAGACCCATGCTGCATCCAGAGACCTCCCTGCCGGGGGATCTCCTGG	165	
DB	78	ACGGGCCCCAACAGACCCATGCTGCATCCAGAGACCTCCCTGCCGGGGGATCTCCTGG	137	
QY	166	CTGTGCTCTGCTCCCTTCCTGGCCACACCTGGGAGAGGTGTGGCCACCCAGCTGCAGG	225	
DB	138	CTGTGCTCTGCTCCCTTCCTGGCCACCCCTGGGAGAGGTGTGGCCACCCAGCTGCAGG	197	
QY	226	ACCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAGGAGATTTCTTCTCCTCCTCCCTGC	285	
DB	198	AGCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAGGAGATTTCTTCTCCTCCTCCCTGC	257	
QY	286	ACAACCGCTCGCAGCTGGTCCAGCCCTCCCTGCTGCATCGGAGGCTGAGCTGGA	345	
DB	258	ACAACCGCTCGCAGCTGGTCCAGCCCTCCCTGCTGCATCGGAGGCTGAGCTGGA	317	

QY	346	GTGACAGCTGGCCCAACTGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCCGA	405	
DB	318	GTGACAGCTGGCCCAACTGCTCAAGCCAGGCGAGCCCTCTGTGGAATCCCAACCCCGA	377	
QY	406	GCTGGCATCCGGCCCTGTGGCGACACCTGCAAGTGGGTGGAACATGACGTGCTGCCG	465	
DB	378	GCTGGCATCCGGCCCTGTGGCGACACCTGCAAGTGGGTGGAACATGACGTGCTGCCG	437	
QY	466	CGGGCTTGGGCTCTTGTGTAAGTGTGCTAGCTATGTTTGCAGAGGGGAGCGGTACA	525	
DB	438	CGGGCTTGGGCTCTTGTGTAAGTGTGCTAGCTATGTTTGCAGAGGGGAGCGGTACA	497	
QY	526	GCACACGGGAGGAGTGTGCTGCAAGCCACCTGCACCCACTACACGAGCTGCTGCT	585	
DB	498	GCACACGGGAGGAGTGTGCTGCAAGCCACCTGCACCCACTACACGAGCTGCTGCT	557	
QY	586	GGGCCACCTCAAGCCAGCTGGGTGTGGGCGGACCTGTGCTCTGCAGGCCAGACAGCA	645	
DB	558	GGGCCACCTCAAGCCAGCTGGGTGTGGGCGGACCTGTGCTCTGCAGGCCAGACAGCA	617	
QY	646	TAGAAGCTTGTGCTGCTACTCTCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAA	705	
DB	618	TAGAAGCTTGTGCTGCTACTCTCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAA	677	
QY	706	TCATCCCTTATAAAGAGGTGCTGTGCTGCTGCACAGCCAGTGTCTCAGGCTGCT	765	
DB	678	TCATCCCTTATAAAGAGGTGCTGTGCTGCTGCACAGCCAGTGTCTCAGGCTGCT	737	
QY	766	TCAAAGCTGGGACCATGAGGGGGCTGTGAGGTCCCGAGGAATCTTGTGCATGA	825	
DB	738	TCAAAGCTGGGACCATGAGGGGGCTGTGAGGTCCCGAGGAATCTTGTGCATGA	797	
QY	826	GCTGCCAGAACCATGAGAGCTCAACATCAGCACCCTGCCACTGCTCCCTGCTGCT	885	
DB	798	GCTGCCAGAACCATGAGAGCTCAACATCAGCACCCTGCCACTGCTCCCTGCTGCT	857	
QY	886	ACACGGGCGAGATGCTCCCAAGTGCAGCTGCAGCTGCAGTGTGCAGGGCGGTTCCGG	945	
DB	858	ACACGGGCGAGATGCTCCCAAGTGCAGCTGCAGTGTGCAGGGCGGTTCCGG	917	
QY	946	AGGAGAGTGTCTGCTGCTGTGACATGGCTACGGGGGAGCCAGTGTGCCACCAAGG	1005	
DB	918	AGGAGAGTGTCTGCTGCTGTGACATGGCTACGGGGGAGCCAGTGTGCCACCAAGG	977	
QY	1006	TGCATTTTCCCTTCCACACCTGTGAGGATCGACGGAGACTGTTTATGTGTCTT	1065	
DB	978	TGCATTTTCCCTTCCACACCTGTGAGGATCGACGGAGACTGTTTATGTGTCTT	1037	
QY	1066	CAGAGGCGAGACCTATTACAGAGCCAGGATGAATGTTCAGAGGAAAGCGGGTGTCTG	1125	
DB	1038	CAGAGGCGAGACCTATTACAGAGCCAGGATGAATGTTCAGAGGAAAGCGGGTGTCTG	1097	
QY	1126	CCAGATCAAGAGCCAGAAAGTGCAGGACATCTCCCTTCTATCTTGGGCGCCCTGAGA	1185	
DB	1098	CCAGATCAAGAGCCAGAAAGTGCAGGACATCTCCCTTCTATCTTGGGCGCCCTGAGA	1157	
QY	1186	CCACCAAGAGGTGACTGACAGTGTTCAGAGACCAAGAACTTCTGATCGGGTCACT	1245	
DB	1158	CCACCAAGAGGTGACTGACAGTGTTCAGAGACCAAGAACTTCTGATCGGGTCACT	1217	
QY	1246	ACAAGACCCCAAGGACTTCTCCCTGGGCCACAGGGGAGACAGGCTTACCAAGTT	1305	
DB	1218	ACAAGACCCCAAGGACTTCTCCCTGGGCCACAGGGGAGACAGGCTTACCAAGTT	1277	
QY	1306	TTGCTTTGGGAGCTGACACCAACACAGGCTGGTGTGGCTGAGTGTGCCATGGGTTT	1365	
DB	1278	TTGCTTTGGGAGCTGACACCAACACAGGCTGGTGTGGCTGAGTGTGCCATGGGTTT	1310	
QY	1366	GCAACTGCTGAGCTGACAGGCTTCAAGTTCAGTTCCTTCAACTGGACAGCAGCTGCA	1425	
DB	1311	GCAACTGCTGAGCTGACAGGCTTCAAGTTCAGTTCCTTCAACTGGACAGCAGCTGCA	1370	

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QY 1426 CCCGAACCGTTACATCTCCAGTTTCCAGGAGCACATCTCCGGTGGGGCCAGGGT 1485
Db 1371 CCCGAACCGTTACATCTCCAGTTTCCAGGAGCACATCTCCGGTGGGGCCAGGGT 1430
QY 1486 CCTGAGGCGCTGACCATGCTCCCTCGCTGCGCTGGGAGCACCGGCTCTGCTTACCTG 1545
Db 1431 CCTGAGGCGCTGACCATGCTCCCTCGCTGCGCTGGGAGCACCGGCTCTGCTTACCTG 1490
QY 1546 TCTGCCCCACCTGCTCTGGAACAAAGGCGCAGGTTAAGACCAATGCTCATGTCCAAAGAGG 1605
Db 1491 TCCGCCACCTGCTCTGGAACAAAGGCGCAGGTTAAGACCAATGCTCATGTCCAAAGAGG 1550
QY 1606 TCTCAGACCTTGCACAAATGCCAGAACTTGGGCAGAGAGAGGCGAGGCGCCAGTGAGGGC 1665
Db 1551 TCTCAGACCTTGCACAAATGCCAGAACTTGGGCAGAGAGAGGCGAGGCGCCAGTGAGGGC 1610
QY 1666 CAGGAGTGAGTGTAGAAAGAACTGGGGCCCTTCGCCCTGCTTTTGGGAAAGATGGG 1725
Db 1611 CAGGAGTGAGTGTAGAAAGAACTGGGGCCCTTCGCCCTGCTTTTGGGAAAGATGGG 1670
QY 1726 CTTCAATTAGATGGCGAAGAGAGAGACACCGCCAGTGGTCCAAAAGGCTCTCTCTTCC 1785
Db 1671 CTTCAATTAGATGGCGAAGAGAGAGACACCGCCAGTGGTCCAAAAGGCTCTCTCTTCC 1730
QY 1786 ACCTGGCCAGACCCCTGTGGGGCAGCGGAGCTTCCCTGTGSCATGAACCCACGGGGTAT 1845
Db 1731 ACCTGGCCAGACCCCTGTGGGGCAGCGGAGCTTCCCTGTGSCATGAACCCACGGGGTAT 1790
QY 1846 TAAATTATGAATCAGCTGAAAAA 1876
Db 1791 TAAATTATGAATCAGCTGAAAAA 1821
```

RESULT 2

us-09-790-264-1/C

Query Match 1.4%; Score 25.8; DB 1; Length 1856;
Best Local Similarity 67.9%; Pred. No. 0;
Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

```
QY 1124 GSCCCAGATCAAGAGCCAGAACTGCGAGGACATCCTCGCCCTTCTATCTGGGCC 1176
Db 1148 GSCCCAGATGAGAGCGGAGATGCTGCACTTCTGGCTCTTGATCTGGGCC 1096
```

Search completed: September 17, 2003, 14:04:57
Job time : 2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 17, 2003, 14:00:33 ; Search time 0.001 Seconds
(without alignments)
202.930 Million cell updates/sec

Title: us-09-944-896-50

Perfect score: 2529

Sequence: 1 MLHPETSPGRGHLAVLLAL.....RNRYICQFAQEHISRWPGS 455

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 446 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : seq264-2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	2447.5	96.8	446	1	us-09-790-264-2

ALIGNMENTS

RESULT 1
us-09-790-264-2

Query Match		96.8%;	Score 2447.5;	DB 1;	Length 446;
Best Local Similarity		97.1%;	Pred. No. 0;		
Matches 442;		Conservative 1;	Mismatches 3;	Indels 9;	Gaps 1;
QY	1	MLHPETSPGRGHLAVLLALIGTTTAEVWPQLOEQAPMAGALNRKESFLLLSLHNRLS	60		
Db	1	MLHPETSPGRGHLAVLLALIGTTAEVWPQLOEQAPMAGALNRKESFLLLSLHNRLS	60		
QY	61	WVQPPADMRRLDWSLSLAQARAALCGIPTPSLASGLWRTLVQVGNMOLLPAGLASF	120		
Db	61	WVQPPADMRRLDWSLSLAQARAALCGIPTPSLASGLWRTLVQVGNMOLLPAGLASF	120		
QY	121	VEVYSLWFAGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC SAGQTAEAFVC	180		
Db	121	VEVYSLWFAGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC SAGQTAEAFVC	180		
QY	181	AYSPGGNWEYNGKTIPIYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNFCRMSQNHG	240		
Db	181	AYSPGGNWEYNGKTIPIYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNFCRMSQNHG	240		
QY	241	RLNISCHCHCPPGYTCGRVCSLQCVHGRFRREECSCVCDIGYGGACATKVHFFPH	300		
Db	241	RLNISCHCHCPPGYTCGRVCSLQCVHGRFRREECSCVCDIGYGGACATKVHFFPH	300		

301 TCDLRIDGDCFMVSSEADTYRARMKCORKGVLQAQIKSQKVDIILAFYLGRLTTEVT 360
|||||
301 TCDLRIDGDCFMVSSEADTYRARMKCORKGVLQAQIKSQKVDIILAFYLGRLTTEVT 360
|||||
361 DSDPETRNFWIGLTYKTAKDSFRWATGEHQAFSTFAFCQPDNDHGLVWLSAAMGFGNCVEL 420
|||||
361 DSDPETRNFWIGLTYKTAKDSFRWATGEHQAFSTFAFCQPDNDHGLVWLSAAMGFGNCVEL 420
|||||
421 QASAAFNWNDQRCCKTRNRYICQFAQEHISRWPGS 455
|||||
412 QASAAFNWNNORCKTRNRYICQFAQEHISRWPGS 446
|||||

Search completed: September 17, 2003, 14:00:33
Job time : 0.001 secs

